

### Amendments to the Specification

Please replace the sequence listing (paper copy and computer readable form thereof) with the attached substitute sequence listing and computer readable form thereof.

Please replace the paragraph which begins on page 5, line 7 and which ends on page 5, line 9, with the following replacement paragraph:

Figure 7 shows a comparison of *thyA* gene products from *E. coli* (SEQ ID NO: 6 having 263 amino acids) [16], *V. cholerae* (SEQ ID NO:4 having 283 amino acids) and *H. influenzae* (SEQ ID NO: 7 having 283 amino acids) [17] showing the high degree of homology between *V. cholerae* and *H. influenzae* compared with *E. coli*.

Please replace the paragraph which begins on page 9, line 32 and which ends on page 10, line 8, with the following replacement paragraph:

The following primers were used for PCR amplification of the insertionally inactivated gene:

ThyA-10: 5'**GCT CTA GAG CCT TAG AAG GCG TGG TTC**' (SEQ ID NO:8)  
corresponding to bases 557 to 575 in SEQ ID NO:2 (Figure 2) with an added *Xba*I site  
(in bold)  
and  
ThyA-11: 5'**GCT CTA GAG CTA CGG TCT TGA TTT ACG GTA T**' (SEQ ID NO:9)  
corresponding to the complementary sequence of bases 235 to 257 in SEQ ID NO:2  
(Figure 3) with an added *Xba*I site (in bold) (Figure 9 + 10)

Please replace the paragraph which begins on page 11, line 3, and which ends on page 11, line 11, with the following replacement paragraph:

Thus the *thyA* gene was further disrupted and the kanamycin resistance gene was also inactivated (by removal of the start of the coding region). The overall result of this procedure was a strain carrying a deleted *thyA* gene that also contained an insertion of noncoding DNA.

ThyA-14: 5'GGG GGC **TCG AGG** GGC ACA TCA CAT GAA<sup>3'</sup> (SEQ ID NO:10)

ThyA-15: 5'CCC CCC **TCG AGC** GCC AGA GTT GTT TCT GAA<sup>3'</sup> (SEQ ID NO:11)

Letters in **bold** indicate *XhoI* cleavage sites (Figure 11).

Please replace the paragraph which begins on page 12, line 17 and which ends on page 13, line 11, with the following replacement paragraph:

From the 5' and 3' regions of the *thyA* locus the following PCR primers were designed:

ThyA-33: 5'GGA **CTA GTG** GGT TTC CTT TTT GCT AT<sup>3'</sup> (SEQ ID NO:12)

corresponding to bases 109 to 126 in the SEQ ID NO:2 (figure 2) (5' region of the *thyA* region) with a *SpeI* site (indicated in bold) and

ThyA-34: 5'CCC CGC **TCG AGA** CCC TAT TTT GCT GCT AC<sup>3'</sup> (SEQ ID NO:13)

corresponding to the complementary sequence of base 815 to 832 in the SEQ ID NO:2 with a *XhoI* site (indicated in bold) attached to it.

This primer pair gives a PCR fragment of 743 bases corresponding to the 5' flanking region of the *thyA* gene.

ThyA-31: 5'CGG **GGT ACC** TGG CTT GAT GGG TTT TAT<sup>3'</sup> (SEQ ID NO:14)

corresponding to bases 22 to 39 in the SEQ ID NO:3 (figure 3) (3' region of the *thyA* region) with a *KpnI* site (indicated in bold) and

ThyA-32: 5'GAA **GGC CTT** CGC CTC TGC TTG CGA CT<sup>3'</sup> (SEQ ID NO:15)

corresponding to the complementary sequence of bases 731 to 749 in the SEQ ID NO:3 with a *StuI* site (indicated in bold)

This primer pair gives a PCR fragment of 746 bases corresponding to the 3' flanking region of the *thyA* gene.

## AMENDMENTS TO THE DRAWINGS

The attached sheet of drawings includes changes to figure 7. This sheet replaces the original sheet of figure 7. In figure 7, the previously omitted sequence identification numbers (SEQ ID NOS:1-3) have been added.

### Attachments:

Replacement sheet

Annotated sheet showing changes